RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/563, 888A_

Source: _IFWO,_

Date Processed by STIC: _7/5/06_

ENTERED

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         RAW SEQUENCE LISTING                  DATE: 07/05/2006
         PATENT APPLICATION:  US/10/563,888A   TIME: 13:54:48

         Input Set : A:\SEQLIST.TXT
         Output Set: N:\CRF4\07052006\J563888A.raw

  4 <110> APPLICANT: Chi-Hong B. Chen
  5        Ralf Landgraf
  7 <120> TITLE OF INVENTION: APTAMERS TO HUMAN EPIDERMAL GROWTH
  8        FACTOR RECEPTOR-3
 10 <130> FILE REFERENCE: 30448108USWO
 12 <140> CURRENT APPLICATION NUMBER: 10/563,888A
 13 <141> CURRENT FILING DATE: 2006-01-09
 15 <150> PRIOR APPLICATION NUMBER: 60/488,679
 16 <151> PRIOR FILING DATE: 2003-07-18
 18 <150> PRIOR APPLICATION NUMBER: PCT/US04/23039
 19 <151> PRIOR FILING DATE: 2004-07-16
 21 <160> NUMBER OF SEQ ID NOS: 20
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 4026
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
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 33 gatgctgaga accaatacca gacactgtac aagctctacg agaggtgtga ggtggtgatg 180
 34 gggaaccttg agattgtgct cacgggacac aatgccgacc tctccttcct gcagtggatt 240
 35 cgagaagtga caggctatgt cctcgtggcc atgaatgaat tctctactct accattgccc 300
 36 aacctccgcg tggtgcgagg gacccaggtc tacgatggga gtttgccat cttcgtcatg 360
 37 ttgaactata acaccaactc cagccacgct ctgcgccagc tccgcttgac tcagctcacc 420
 38 gagattctgt caggggggtgt ttatattgag aagaacgata agctttgtca catggacaca 480
 39 attgactgga gggacatcgt gagggaccga gatgctgaga tagtggtgaa ggacaatggc 540
 40 agaagctgtc cccctgtca tgaggtttgc aaggggcgat gctggggtcc tggatcagaa 600
 41 gactgccaga cattgaccaa gaccatctgt gctcctcagt gtaatggtca ctgctttggg 660
 42 cccaacccca accagtgctg ccatgatgag tgtgccgggg gctgctcagg ccctcaggac 720
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58 cgagaatttg cccatgaggc cgaatgcttc tcctgccacc cggaatgcca acccatgggg 1680
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61 tacaagtacc cagatgttca gaatgaatgt cggccctgcc atgagaactg cacccagggg 1860
62 tgtaaaggac cagagcttca agactgttta ggacaaacac tggtgctgat cggcaaaacc 1920
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79 ctagccaatg agttcaccag gatggcccga gacccaccac ggtatctggt cataaagaga 2940
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96 caggccccccc atgtccatta tgcccgccta aaaactctac gtagcttaga ggctacagac 3960
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101 <211> LENGTH: 1342
102 <212> TYPE: PRT
103 <213> ORGANISM: Homo sapiens
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110 Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
111          35                   40                   45
112 Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
113          50                   55                   60
114 Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
115 65                   70                   75                   80
116 Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
117          85                   90                   95
118 Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
119          100                  105                  110
120 Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
121          115                  120                  125
122 His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
123          130                  135                  140
124 Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
125 145                  150                  155                  160
126 Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
127          165                  170                  175
128 Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
129          180                  185                  190
130 Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
131          195                  200                  205
132 Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
133          210                  215                  220
134 Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
135 225                  230                  235                  240
136 Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
137          245                  250                  255
138 Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
139          260                  265                  270
140 Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
141          275                  280                  285
142 Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
143          290                  295                  300
144 Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
145 305                  310                  315                  320
146 Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
147          325                  330                  335
148 Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
149          340                  345                  350
150 Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
151          355                  360                  365
152 Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
153          370                  375                  380
154 Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
155 385                  390                  395                  400
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157             405             410             415
158 Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile
159             420             425             430
160 Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
161         435             440             445
162 Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
163     450             455             460
164 His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
165 465             470             475             480
166 Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
167             485             490             495
168 Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
169         500             505             510
170 Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
171         515             520             525
172 Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
173     530             535             540
174 His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Gly
175 545             550             555             560
176 Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
177             565             570             575
178 Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
179         580             585             590
180 Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
181         595             600             605
182 Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
183     610             615             620
184 Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr
185 625             630             635             640
186 His Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe
187             645             650             655
188 Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln
189         660             665             670
190 Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu
191         675             680             685
192 Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe
193         690             695             700
194 Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe
195 705             710             715             720
196 Gly Thr Val His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys
197             725             730             735
198 Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser
199         740             745             750
200 Phe Gln Ala Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His
201         755             760             765
202 Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln
203         770             775             780
204 Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg
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205 785                      790                  795                    800
206 Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val
207                  805                  810                  815
208 Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His
209                  820                  825                  830
210 Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val
211          835                  840                  845
212 Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys
213      850                  855                  860
214 Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu
215 865                  870                  875                  880
216 Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser
217                  885                  890                  895
218 Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr
219              900                  905                  910
220 Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu
221          915                  920                  925
222 Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met
223      930                  935                  940
224 Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu
225 945                  950                  955                  960
226 Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu
227                  965                  970                  975
228 Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro
229              980                  985                  990
230 His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu
231          995                  1000                 1005
232 Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala Thr
233      1010                 1015                 1020
234 Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu Asn Arg
235 1025                 1030                 1035                 1040
236 Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly Tyr Met Pro
237              1045                 1050                 1055
238 Met Asn Gln Gly Asn Leu Gly Gly Ser Cys Gln Glu Ser Ala Val Ser
239          1060                 1065                 1070
240 Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser Leu His Pro Met Pro
241          1075                 1080                 1085
242 Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu Gly His Val Thr Gly Ser
243      1090                 1095                 1100
244 Glu Ala Glu Leu Gln Glu Lys Val Ser Met Cys Arg Ser Arg Ser Arg
245 1105                 1110                 1115                 1120
246 Ser Arg Ser Pro Arg Pro Arg Gly Asp Ser Ala Tyr His Ser Gln Arg
247              1125                 1130                 1135
248 His Ser Leu Leu Thr Pro Val Thr Pro Leu Ser Pro Pro Gly Leu Glu
249          1140                 1145                 1150
250 Glu Glu Asp Val Asn Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly
251          1155                 1160                 1165
252 Thr Pro Ser Ser Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser
253      1170                 1175                 1180
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; N Pos. 35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54
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Seq#:14; N Pos. 75,76,77,78,79,80,81,82,83

VERIFICATION SUMMARY   DATE: 07/05/2006
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L:727 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:731 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:732 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14